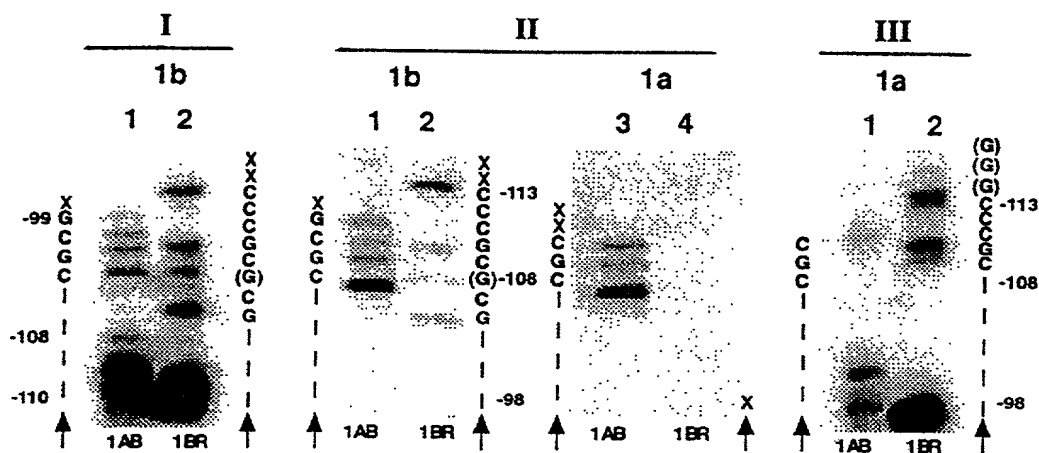


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-113 -108 -99

1a 5'-----TTTGGGCG (T) GCGGGGCGAAGAC-----3'

X← 1BR 5'

1b 5'-----TTTGGGCG (T) GCGGGGCGAGAC-----3'

XXXCCCGC (G) CGGGGGCGC← 1BR 5'

I' and II'

1a 3'-----AAACCCGC (A) CGGGGGCGTTCTG-----5'

5' 1AB CG (C) GCGGGGCGXX

1b 3'-----AAACCCGC (A) CGGGGGCGCTCTG-----5'

5' 1AB CG (C) GCGGGGCGX X

III'

-113 -108 -99

1a 5'-----TTTGGGCG (T) GCGGGGCG (A) AGAC-----3'

AAACCCGC (G) CGGGGGCG (C) ← 1BR 5'

Figure 1

PRIMER-SPECIFIC AND MISPAIR EXTENSION
ASSAY FOR IDENTIFYING GENE VARIATION

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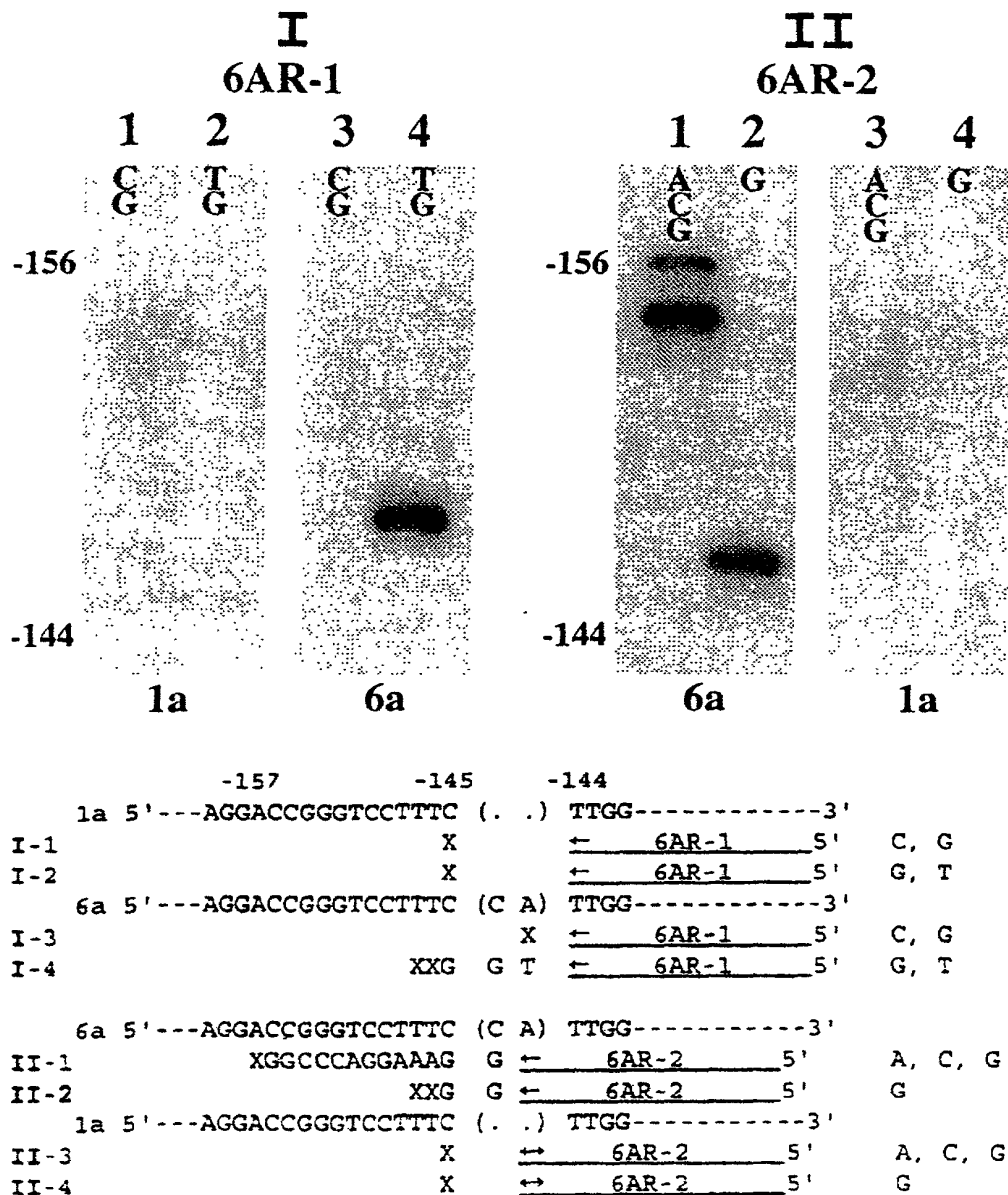


FIG. 2

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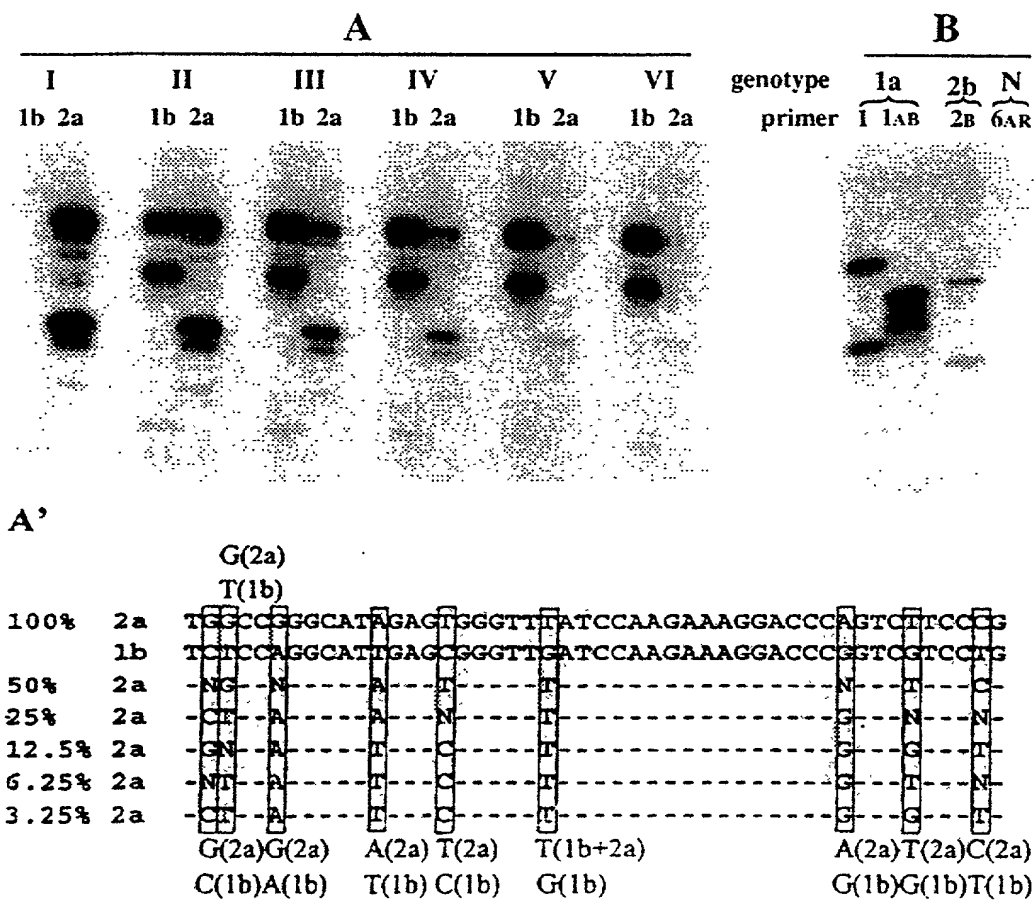


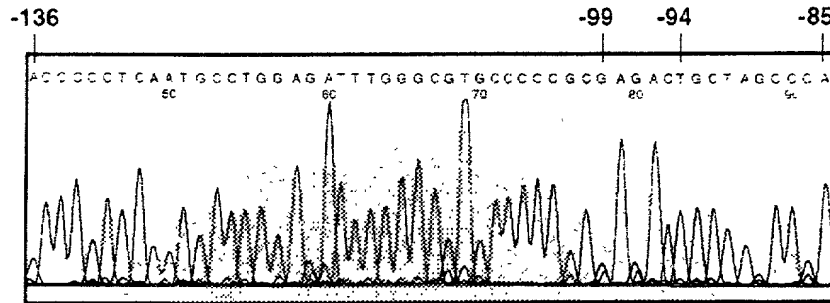
FIG. 3

PRIMER-SPECIFIC AND MISPAIR EXTENSION
ASSAY FOR IDENTIFYING GENE VARIATION

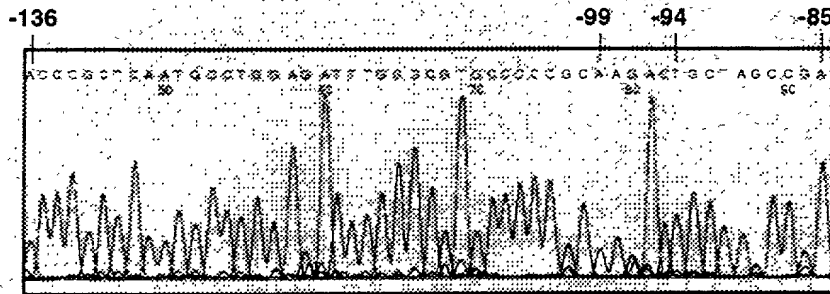
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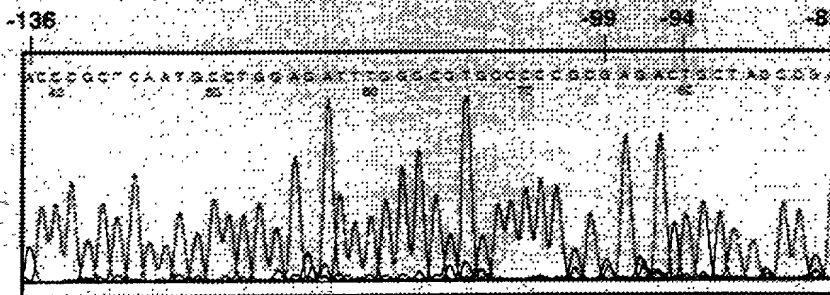
I J
(1b)



H
(1a)



I
(1b)



II

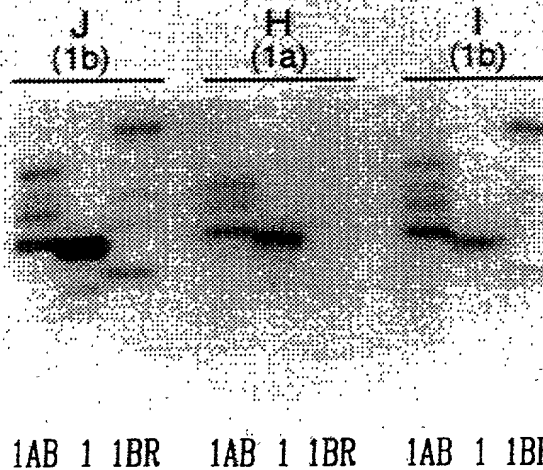
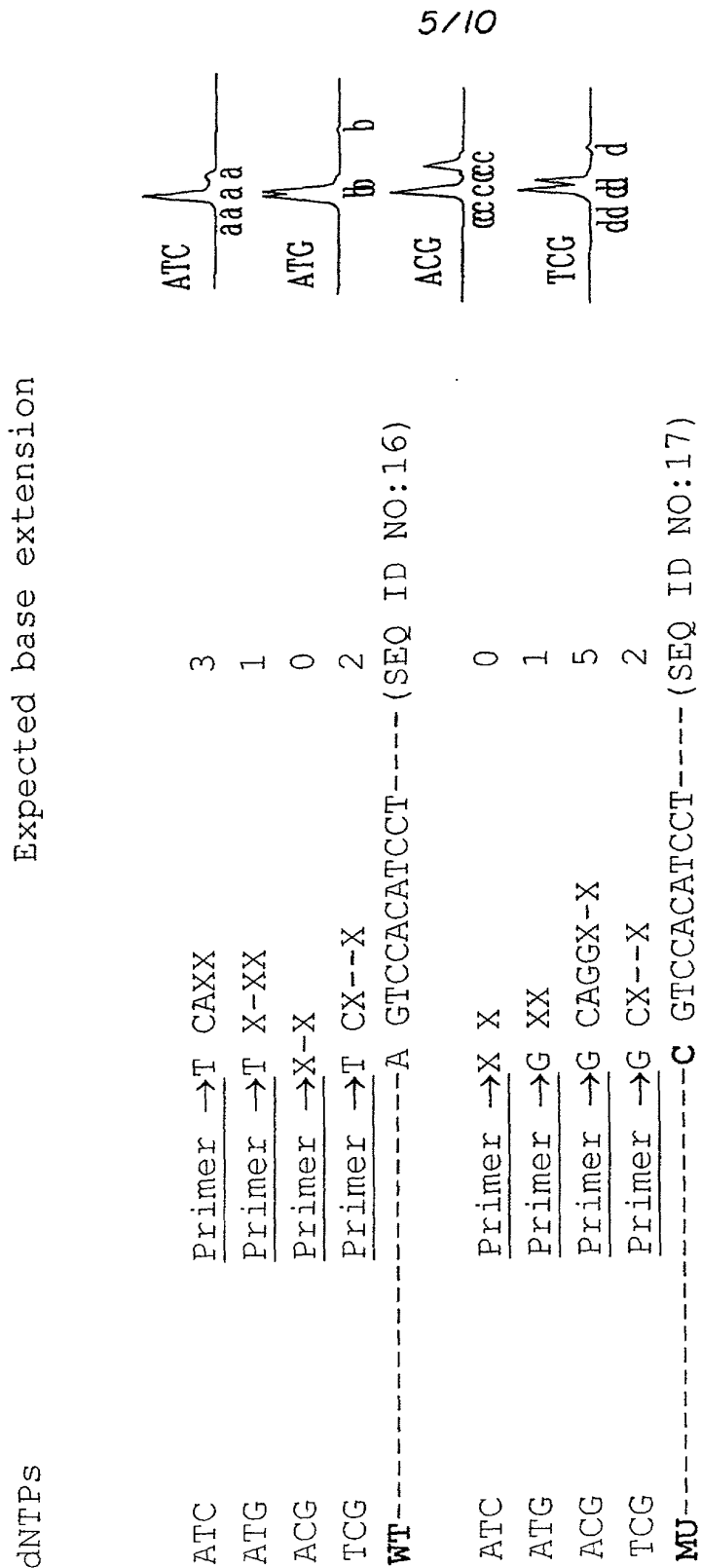


FIG. 4



WT-5B

MU-5A

FILE EA

PRIMER-SPECIFIC AND MISPAIR EXTENSION
ASSAY FOR IDENTIFYING GENE VARIATION

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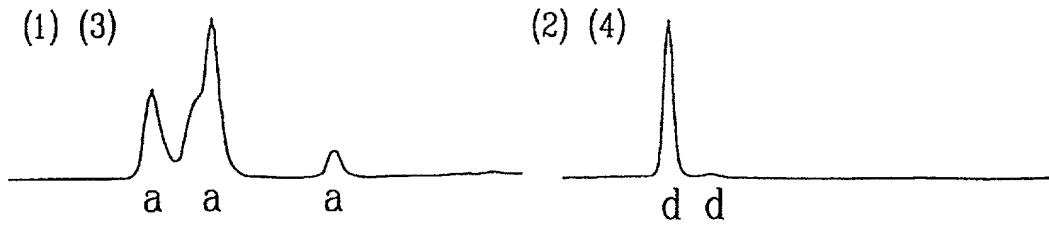


FIG. 1

3'	XXAGACTTCTGAGTCTAA ¹ CAACGTGAAATTTA	5' PRO90L-R	(1)	(SEQ ID NO: 24)
5'	--AATCTGAAGACTCAGATTGGTTGCACTTTAAAT--	3' L90	(SEQ ID NO: 25)	
X				
3'	TTCTGAGTCTAACCAACGTGAAATTTA	5' PRO90L-R	(2)	(SEQ ID NO: 26)
5'	--AATCTGATGACTCAGATTGGTTGCACTTTAAAT--	3' L90M	(SEQ ID NO: 27)	
5'	CTGTCAACATAATTGGAAGAAATCTGATGACGAGAXX	3' PRO90M-F	(3)	(SEQ ID NO: 28)
3'	--GACAGTTGTATTAAACCTTCTTTAGACTACTGCGTCTAA--	5' L90M	(SEQ ID NO: 29)	8/10
X				
5'	CTGTCAACATAATTGGAAGAAATCTGAT	3' PRO90M-F	(4)	(SEQ ID NO: 30)
3'	--GACAGTTGTATTAAACCTTCTTTAGACAACCTGAGTCTAA--	5' L90	(SEQ ID NO: 31)	

PRIMER-SPECIFIC AND MISPAIR EXTENSION
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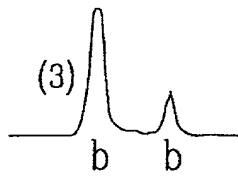
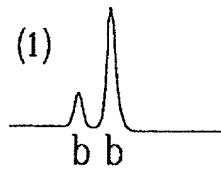
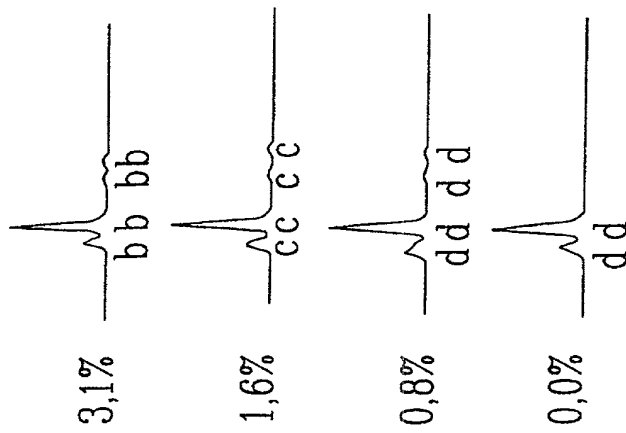


FIG. 7B

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MU → T AGTTGTATTAAXX (SEQ ID NO: 32)
----- A TCAACATAATTGGAAGA (SEQ ID NO: 33)

→ X
----- G -----

FIG. 10